hydrogen-bond with hydrogen bonding groups in the biopolymer;

covering possible docking structures between said biopolymer and said ligand while changing the conformation of said ligand; wherein matching of distances among dummy atoms and those among heteroatoms of the ligand are tested; and

outputting information about three-dimensional coordinates for each atom of the ligand in one or more stable docking structures including the most stable one relative to the biopolymer; as well as the stability of said docking structures, the binding modes and conformations of the ligand in said structures.

7. (Amended) A method for determining stable ligand-biopolymer docking structures comprising:

inputting three-dimensional coordinates for each atom of a biopolymer as well as atomic element, bond-type of covalent bonds and three-dimensional coordinates for each atom of a ligand; wherein dummy atoms are preset at the positions of heteroatoms that can hydrogen-bond with hydrogen-bonding groups in the biopolymer;

selecting stable docking structures between said biopolymer and said ligand while changing the conformation of said ligand; wherein matching of distances among dummy atoms and those among heteroatoms of the ligand are tested; and

outputting information about three-dimensional coordinates for each atom of the ligand in one or more stable docking structures including the most stable one relative to the biopolymer, as well as the stability of said docking structures, the binding modes and conformations of the ligand in said structures.

8. (Amended) A method for determining stable ligand-biopolymer docking structures comprising:

inputting three-dimensional coordinates for each atom of a biopolymer as well as

atomic element, bond-type of covalent bonds and three-dimensional coordinates for each atom of a ligand, wherein dummy atoms are preset at positions of atoms that can specifically interact with functional groups in the biopolymer;

covering possible docking structures between said biopolymer and said ligand while changing the conformation of said ligand, wherein matching of distances among dummy atoms and those among atoms of the ligand are tested; and

outputting information about three-dimensional coordinates for each atom of the ligand in one or more stable docking structures including the most stable one relative to the biopolymer, as well as the stability of said docking strutures, the binding modes and conformations of the ligand in said structures.

9. (Amended) A method for determining stable ligand-biopolymer docking structures comprising:

inputting three-dimensional coordinates for each atom of a biopolymer as well as atomic element, bond-type of covalent bonds and three-dimensional coordinates for each atom of a ligand, wherein dummy atoms are preset at positions of atoms that can specifically interact with functional groups in the biopolymer;

selecting stable docking structures between said biopolymer and said ligand while changing the conformation of said ligand, wherein matching of distances among dummy atoms and those among atoms of the ligand are tested; and

outputting information about three-dimensional coordinates for each atom of the ligand in one or more stable docking structures including the most stable one relative to the biopolymer, as well as the stability of said docking structures, the binding modes and conformations of the ligand in said structures.

10. (Amended) A method for estimating stable docking structures between a

biopolymer and a ligand, comprising selecting stable docking structures by matching of distances among dummy atoms and those among heteroatoms of the ligand, said dummy atoms being preset at the positions of heteroatoms of the ligand that can be hydrogen-bonded with hydrogen bonding groups in the biopolymer.

11. (Amended) A method for estimating stable docking structures between a biopolymer and a ligand, comprising selecting stable docking structures by matching of distances among dummy atoms and those among atoms of the ligand, said dummy atoms being preset at the positions of atoms of the ligand that can specifically interact with functional groups in the biopolymer, while changing the conformation of the ligand.--

C1 Cont

IN THE ABSTRACT

Applicants provide herewith the Abstract that was inadvertently not received by the Examiner in the previous response. Its entry in place of the original Abstract is respectfully requested.

SUPPORT FOR AMENDMENTS

Claims 6-11 are now active in this application. These claims are supported by the specification and claims as originally filed. The new Abstract provided is likewise supported by the original application as filed and obviates the Examiner's objection to the Abstract. No new matter has been added by these amendments.

REQUEST FOR RECONSIDERATION

Applicants representative would like to thank Examiner Borin for the courteous and helpful discussion regarding the present application. As noted during that discussion, the

Examiner has agreed to withdraw the rejection under 35 U.S.C. 101. Further, the Examiner indicated that a primary issue was the ordering of the various limitations in the claims. This is believed to be addressed in the above amendments.

The present invention provides methods for the determination of the most energetically favorable docking structures between a biopolymer (such as a protein) and a ligand having one or more atoms that can interact with functional groups in the biopolymer, or one or more hydrogen bonding heteroatoms. An important factor in each claim is that these atoms or heteroatoms in the ligand that either interact with functional groups in the biopolymer or provide hydrogen bonding sites are each designated to correspond to a dummy atom. Hence the dummy atoms used in the present method correspond in space to the atom or heteroatom itself. Also, there can be multiple dummy atoms in the present method, since the ligand can have multiple atoms that interact with biopolymer functional groups or multiple hydrogen bonding heteroatoms present (see figures).

The claims stand rejected under 35 U.S.C. 101. As noted above, the Examiner has agreed to withdraw this rejection, for which Applicants express their appreciation.

The claims also stand rejected under 35 U.S.C. 112, first and second paragraph. This rejection has been obviated by the above amendments and where not obviated is respectfully traversed on the grounds that the claims as stated are clear and definite. Certain of the claims recite a step of "covering" the docking structures. These claims require that the program look at all or nearly all permutations of docking structures between the ligand and biopolymer, given the specified dummy atoms and their general areas of interaction. Alternatively, other claims require the selection of "stable docking structures" followed by varying certain parameters, to determine an ultimate most stable structure. Whether the terms "covering" or "selecting" are or are not explicitly used in the text, their meanings are clear and described in the text of the application. In particular, at page 14, lines 4-5, the specification indicates that the present methods permit one to search all possible docking structures in a short time (i.e. covering possible docking structures). The use of a group of stable docking structures to determine the most stable (i.e. by selecting stable docking structures) is described in the text at pages 24-26.

Accordingly, the rejections are believed to be overcome and should be withdrawn.

Applicants submit that the application is now in condition for allowance, and early notification of such action is earnestly solicited.

Respectfully submitted,

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